

**Table S4**

**Repeats identified *de novo* by cross-match alignment in *S. sclerotiorum* and *B. cinerea* genomes.**

	<i>S. sclerotiorum</i>	<i>B. cinerea</i> B05.10	<i>B. cinerea</i> T4
Total repeats*	23,036	5,341	3,408
Average length	574	778	749
Repeat families <sup>#</sup>	1,984	1,484	1,122
Repeat regions <sup>^</sup>	2,694	1,778	1,415
Repeat region length (bp)	1,043	949	871
Total repeat (bp)	2,940,585	1,712,362	1,237,959
Assembly size (bp)	38,001,451	38,786,820	37,887,277
% repeat of assembly	7.7%	4.4%	3.3%

\*Total repeats are the repeat units identified by cross\_match

#Repeat families are identity-clustered repeat units

<sup>^</sup>Repeat regions merge overlapping repeat units into a single region